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RAW SEQUENCE LISTING

DATE: 06/21/2002

PATENT APPLICATION: US/10/055,001A

TIME: 14:57:56

Input Set : A:\Sequence.txt

Output Set: N:\CRF3\06212002\J055001A.raw

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6 <110> APPLICANT: Wesley, Susan V.
7      Waterhouse, Peter
8      Helliwell, Christopher A.
10 <120> TITLE OF INVENTION: Method and means for producing efficient silencing
constructs
11      using recombinational cloning
13 <130> FILE REFERENCE: HELLGA
C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/055,001A
C--> 15 <141> CURRENT FILING DATE: 2002-06-11
15 <160> NUMBER OF SEQ ID NOS: 26
17 <170> SOFTWARE: PatentIn version 3.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 25
22 <212> TYPE: DNA
23 <213> ORGANISM: Artificial sequence
25 <220> FEATURE:
26 <223> OTHER INFORMATION: core sequence of recombination site attB1
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33 <211> LENGTH: 25
34 <212> TYPE: DNA
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37 <220> FEATURE:
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44 <210> SEQ ID NO: 3
45 <211> LENGTH: 25
46 <212> TYPE: DNA
47 <213> ORGANISM: Artificial sequence
49 <220> FEATURE:
50 <223> OTHER INFORMATION: core sequence of recombination site attB3
52 <400> SEQUENCE: 3
53 acccagcttt cttgtacaaa cttgt                                25
56 <210> SEQ ID NO: 4
57 <211> LENGTH: 25
58 <212> TYPE: DNA
59 <213> ORGANISM: Artificial sequence
61 <220> FEATURE:
62 <223> OTHER INFORMATION: core sequence of recombination site attR1
64 <400> SEQUENCE: 4
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68 <210> SEQ ID NO: 5

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69 <211> LENGTH: 25
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71 <213> ORGANISM: Artificial sequence
73 <220> FEATURE:
74 <223> OTHER INFORMATION: core sequence of recombination site attr2
76 <400> SEQUENCE: 5
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80 <210> SEQ ID NO: 6
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82 <212> TYPE: DNA
83 <213> ORGANISM: Artificial sequence
85 <220> FEATURE:
86 <223> OTHER INFORMATION: core sequence of recombination site attr3
88 <400> SEQUENCE: 6
89 gttcagcttt cttgtacaaa gttgg 25
92 <210> SEQ ID NO: 7
93 <211> LENGTH: 25
94 <212> TYPE: DNA
95 <213> ORGANISM: Artificial sequence
97 <220> FEATURE:
98 <223> OTHER INFORMATION: core sequence of recombination site attL1
100 <400> SEQUENCE: 7
101 agcctgcttt tttgtacaaa gttgg 25
104 <210> SEQ ID NO: 8
105 <211> LENGTH: 25
106 <212> TYPE: DNA
107 <213> ORGANISM: Artificial sequence
109 <220> FEATURE:
110 <223> OTHER INFORMATION: core sequence of recombination site attL2
112 <400> SEQUENCE: 8
113 agcctgcttt cttgtacaaa gttgg 25
116 <210> SEQ ID NO: 9
117 <211> LENGTH: 25
118 <212> TYPE: DNA
119 <213> ORGANISM: Artificial sequence
121 <220> FEATURE:
122 <223> OTHER INFORMATION: core sequence of recombination site attL3
124 <400> SEQUENCE: 9
125 acccagcttt cttgtacaaa gttgg 25
128 <210> SEQ ID NO: 10
129 <211> LENGTH: 25
130 <212> TYPE: DNA
131 <213> ORGANISM: Artificial sequence
133 <220> FEATURE:
134 <223> OTHER INFORMATION: core sequence of recombination site attP1
136 <400> SEQUENCE: 10
137 gttcagcttt tttgtacaaa gttgg 25
140 <210> SEQ ID NO: 11
141 <211> LENGTH: 25

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142 <212> TYPE: DNA
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145 <220> FEATURE:
146 <223> OTHER INFORMATION: core sequence of recombination site attP2,P3
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149 gttcagcttt cttgtacaaa gttgg                               25
152 <210> SEQ ID NO: 12
153 <211> LENGTH: 1188
154 <212> TYPE: DNA
155 <213> ORGANISM: Artificial sequence
157 <220> FEATURE:
158 <223> OTHER INFORMATION: cDNA sequence of the Arabidopsis thaliana chalcone synthase
codin
159      g region
161 <400> SEQUENCE: 12
162 atggtgatgg ctggtgcttc ttctttggat gagatcagac aggtcagag agctgatgga      60
163 cctgcaggca tcttggtctat tggcactgct aacctgaga accatgtgct tcaggcggag      120
164 tctcctgact actacttccg catcaccaac agtgaacaca tgaccgacct caaggagaag      180
165 ttcaagcgca tgtgcgacaa gtcgacaatt cggaaacgtc acatgcatct gacggaggaa      240
166 ttctctcaag aaaaccacaca catgtgtgct tacatggctc cttctctgga caccagacag      300
167 gacatcgctg tggtcgaagt ccctaagcta ggcaaagaag cggcagtga ggccatcaag      360
168 gagtggggcc agcccaagtc aaagatcact catgtcgtct tctgcactac ctccggcgctc      420
169 gacatgcctg gtgctgacta ccagctcacc aaagcttctt gtctccgtcc ttccgtcaag      480
170 cgtctcatga tgtaccagca aggttgcttc gccggcggta ctgtcctccg tatcgctaag      540
171 gatctgcgag agaacaaccg tggagcacgt gtctctgctt tctgctctga gatcacagcc      600
172 gttaccttcc gtggctccctc tgacaccac cttgactccc tegtccgtca ggctcttttc      660
173 agtgatggcg ccgccgcact cattgtgggg tcggaccctg acacatctgt cggagagaaa      720
174 cccatctttg agatgggtgtc tgcgcgtcag accatccttc cagactctga tgggtgccata      780
175 gacggacatt tgagggaagt tggctctacc ttccatctcc tcaaggatgt tcccggcctc      840
176 atctccaaga acattgtgaa gagtctagac gaagcgttta aacctttggg gataagtga      900
177 tgaactccc tcttctggat agcccacct ggaggtccag cgatcctaga ccaggtggag      960
178 ataaagctag gactaaagga agagaagatg agggcgacac gtcacgtgtt gagcgagtat     1020
179 ggaacatgt cgagcgcgtg cgttctcttc atactagacg agatgaggag gaagtcagct     1080
180 aaggatggg tggccacgac aggagaaggg ttggagtggg gtgtcttgtt tggtttcgga     1140
181 ccaggtctca ctggttagac agtcgtcttg cacagcgttc ctctctaa      1188
184 <210> SEQ ID NO: 13
185 <211> LENGTH: 18691
186 <212> TYPE: DNA
187 <213> ORGANISM: Artificial sequence
189 <220> FEATURE:
190 <223> OTHER INFORMATION: acceptor vector pHELLSGATE
192 <220> FEATURE:
193 <221> NAME/KEY: misc_feature
194 <222> LOCATION: (7922)..(9985)
195 <223> OTHER INFORMATION: spectinomycin resistance
197 <220> FEATURE:
198 <221> NAME/KEY: misc_feature
199 <222> LOCATION: (10706)..(11324)
200 <223> OTHER INFORMATION: right T-DNA border fragment
202 <220> FEATURE:

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203 <221> NAME/KEY: misc_feature
204 <222> LOCATION: (11674)..(13019)
205 <223> OTHER INFORMATION: CaMV35S promoter fragment
207 <220> FEATURE:
208 <221> NAME/KEY: misc_feature
209 <222> LOCATION: (17890)..(17659)
210 <223> OTHER INFORMATION: attP1 recombination site (complement)
212 <220> FEATURE:
213 <221> NAME/KEY: misc_feature
214 <222> LOCATION: (17610)..(16855)
215 <223> OTHER INFORMATION: ccdB selection marker (complement)
217 <220> FEATURE:
218 <221> NAME/KEY: misc_feature
219 <222> LOCATION: (16551)..(16319)
220 <223> OTHER INFORMATION: attP2 recombination site (complement)
222 <220> FEATURE:
223 <221> NAME/KEY: misc_feature
224 <222> LOCATION: (14660)..(16258)
225 <223> OTHER INFORMATION: pdk2 intron 2
227 <220> FEATURE:
228 <221> NAME/KEY: misc_feature
229 <222> LOCATION: (15002)..(15661)
230 <223> OTHER INFORMATION: chloramphenicol resistance gene
232 <220> FEATURE:
233 <221> NAME/KEY: misc_feature
234 <222> LOCATION: (14387)..(14619)
235 <223> OTHER INFORMATION: attP2 recombination site
237 <220> FEATURE:
238 <221> NAME/KEY: misc_feature
239 <222> LOCATION: (13675)..(13980)
240 <223> OTHER INFORMATION: ccdB selection marker (complement)
242 <220> FEATURE:
243 <221> NAME/KEY: misc_feature
244 <222> LOCATION: (13048)..(13279)
245 <223> OTHER INFORMATION: attP1 recombination site
247 <220> FEATURE:
248 <221> NAME/KEY: misc_feature
249 <222> LOCATION: (17922)..(18687)
250 <223> OTHER INFORMATION: octopine synthase gene terminator region
252 <220> FEATURE:
253 <221> NAME/KEY: misc_feature
254 <222> LOCATION: (264)..(496)
255 <223> OTHER INFORMATION: nopaline synthase gene promoter
257 <220> FEATURE:
258 <221> NAME/KEY: misc_feature
259 <222> LOCATION: (497)..(1442)
260 <223> OTHER INFORMATION: nptII coding region
262 <220> FEATURE:
263 <221> NAME/KEY: misc_feature

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264 <222> LOCATION (1443)..(2148)
 265 <223> OTHER INFORMATION: nopaline synthase gene terminator
 267 <220> FEATURE:
 268 <221> NAME/KEY: misc_feature
 269 <222> LOCATION: (2149)..(2706)
 270 <223> OTHER INFORMATION: a left T-DNA border region
 272 <400> SEQUENCE: 13

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273 ggcgcacta gtgatatccc ggggccatgg cggccgggag catgcgacgt cgggcccacat    60
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275 gaaaacctcg gcgttaccga acttaatcgc ctggcagcac atcccccttt cgcagctgg    180
276 cgtaatagcg aagaggcccg caccgatcgc ctttcccaac agttgcgcag cctgaatggc    240
277 gaatggaaat tgtaaacggt aatgggtttc tggagtttaa tgagctaagc acatacgtca    300
278 gaaaccatta ttgcgcgttc aaaagtcgcc taaggctact atcagctagc aaatatttct    360
279 tgtcaaaaat gctccactga cgttccataa attccccctg gtatccatt agagtctcat    420
280 attcactctc aatccaaata atctgcaatg gcaattacct tatccgcaac ttctttacct    480
281 atttccgccc ggatccgggc aggttctccg gccgcttggg tggagaggct attcggctat    540
282 gactgggcac aacagacaat cggctgctct gatgccgcgc tgttccggct gtcagcgcag    600
283 gggcgcgcgc ttctttttgt caagaccgac ctgtccgggt cctgaatga actgcaggac    660
284 gaggcagcgc ggtatcgtg gctggccacg acgggcgttc cttgcgcagc tgtgctcgac    720
285 ttgttcactg aagcgggaag ggactggctg ctattgggcg aagtgcgcgg gcaggatctc    780
286 ctgtcatctc accttgctcc tgcgcagaaa gtatccatca tggctgatgc aatgcggcgg    840
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288 cgagcacgta ctcggtatga agccggtctt gtcgatcagg atgatctgga cgaagagcat    960
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291 ttttctggat tcatcgactg tggccggctg ggtgtggcgg accgctatca ggacatagcg    1140
292 ttggctaccc gtgatatctg tgaagagctt ggcggcgaat gggctgaccg ctctcctcgt    1200
293 ctttacggtg tcgcgcgtcc cgtatcgagc cgcctgcct tctatgcct tcttgacgag    1260
294 ttcttctgag cgggactctg ggggttcgaaa tgaccgacca agcgacgcc aacctgccat    1320
295 cagcagatct cgtatccacc gccgccttct atgaaagggt gggcttcgga atcgtttcc    1380
296 gggacgcgcg ctggatgatc ctccagcgcg gggatctcat gctggagttc ttcgcccacc    1440
297 ccgatccaac acttacgttt gcaacgtcca agagcaaata gaccacgaac gccggaagggt    1500
298 tgccgcagcg tgtggattgc gtctcaattc tctcttgagc gaatgcaatg atgaatatga    1560
299 tactgactat gaaactttga gggataactg cctagcaccg tcacctcata acgtgcatca    1620
300 tgcctgccct gacaacatgg aacatcgcta ttttctgaa gaattatgct cgttggagga    1680
301 tgtcgcggca attgcagcta ttgccaacat cgaactaccc ctacgcctg cattcatcaa    1740
302 tattattcat gcggggaaag gcaagattaa tccaactggc aaatcatcca gcgtgattgg    1800
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305 ttcttaagat tgaatcctgt tgccggtctt gcgatgatta tcatataatt tctgttgaat    1980
306 tacgttaagc atgtaataat taacatgtaa tgcatgacgt tatttatgag atgggttttt    2040
307 atgattagag tcccgcaatt atacatttaa tacgcgatag aaaacaaaat atagcgcgca    2100
308 aactaggata aattatcgcg cgcggtgtca tctatgttac tagatcgaat taattccagg    2160
309 cgggtgaagg caatcagctg ttgccgctct cactggtgaa aagaaaaacc accccagtac    2220
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311 tatatcctgc caccagccag ccaacagctc cccgaccggc agctcggcac aaaatcacca    2340
312 ctogatacag gcagcccatc agtcggggac ggcgtcagcg ggagagccgt tgtaaggcgg    2400
313 cagactttgc tcatgttacc gatgctatc ggaagaacgg caactaagct gccgggtttg    2460
314 aaacacggat gatctcgcgg agggtagcat gttgattgta acgatgacag agcgttgctg    2520

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VERIFICATION SUMMARY

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L 15 M 270 C: Current Application Number differs, Replaced Current Application No

L 15 M 271 C: Current Filing Date differs, Replaced Current Filing Date